# *Metarhizium puerense* (Hypocreales, Clavicipitaceae): a new species from Yunnan, south-western China

Jin Mei Ma<sup>‡</sup>, Zhi Qin Wang<sup>‡</sup>, Zhi Li Yang<sup>‡</sup>, Yue Chen<sup>‡</sup>, Song Yu Li<sup>‡</sup>, Hong Yu<sup>‡,‡</sup>

‡ School of Ecology and Environment, Yunnan University, Kunming, China

Corresponding author: Hong Yu (<u>hongyu@ynu.edu.cn</u>) Academic editor: Ning Jiang

# Abstract

## Background

As a genus within the Clavicipitaceae, *Metarhizium* exhibits rich morphological and ecological diversity, with a wide distribution and a variety of hosts. Currently, sixty-eight species of *Metarhizium* have been described.

#### New information

A new species of *Metarhizium*, *M. puerense* (Hong Yu bis), was described in Pu'er City, Yunnan Province, south-western China. Based on morphological characteristics and multilocus phylogenetic analyses, *Metarhizium puerense* was confirmed to be phylogenetically related to *M. album*, but was clearly separated and formed a distinct branch. In contrast, the host of *Metarhizium album* was plants and leafhoppers and that lepidopteran larvae were the host of *M. puerense*. The diagnostic features of *M. puerense* were solitary to multiple stromata and smooth-walled, cylindrical with rounded apices conidia.

# Keywords

Metarhizium, morphology, phylogenetic analyses

# Introduction

*Metarhizium*, as a group with rich morphological and ecological diversity in Clavicipitaceae, is very rich in widely distributed and complex habitats (Bischoff et al.

2009). The type species Metarhizium anisopliae (Metschn 1879) was used by Sorokin (1883) to establish the new asexual genus Metarhizium (Tulloch 1976). Advances in molecular systematics have led to the emergence of multigene systematic analysis as a new technical method for the taxonomic identification of *Metarhizium* sp., combining functional protein genes with rDNA gene fragments (Sung et al. 2007, Kepler et al. 2012, Kepler et al. 2014). In their study of genetic diversity within Metarhizium species, Driver et al. (2000) were the first to utilise molecular biology techniques. They solved the problem of classification at the species and varietal levels by identifying four variants in the M etarhizium anisopliae complex groups, five variants in the M. flavoviride (Gams 1973) complex groups and delineating *M. album* (Petch 1931). In a multi-gene phylogenetic study of Metarhizium anisopliae and M. flavoviride lineages, Bischoff et al. 2006 and Bischoff et al. 2009 elevated and accepted Metarhizium varieties to species rank by using additional protein-coding genes (*EF-1a*, *RPB1*, *RPB2* and TUB). The reexamination of Metarhizium and related genera led to the establishment of six new genera: Keithomyces, Marquandomyces, Papiliomyces, Purpureomyces, Sungia and Yosiokobayasia (Mongkolsamrit et al. 2020). Chamaeleomyces (Samson 1974) and Nomuraea spp. (Samson 1974), excluding N. atypicola (Samson 1974) and Paecilomyces viridis (Segretain 1964), were transferred to Metarhizium, and 19 new species of Metarhizium were reported. Other new species have been reported by Chen et al. (2018a), Chen et al. (2018b), Chen et al. (2018c), Chen et al. (2023) and Li et al. (2023). Currently, sixty-eight species of Metarhizium have been described.

According to the latest classification system, the *Metarhizium* genus belongs to the Fungi, Ascomvcota. Sordariomvcetes. Hypocreales and Clavicipitaceae. Its tvpical morphological characteristics are: Sexual form: Stromata single or multiple, unbranched or irregularly branched, mostly fleshy, with the main colours being pale yellow, green to greenish-brown or dark purple; fertile parts columnar or rod-shaped; perithecia partially or completely immersed; asci mainly columnar, ascospores linear, fusiform, breaking into secondary ascospores upon maturity or not. Asexual form: Growing rapidly on PDA medium, the colonies are flat and velvety, initially white and turn yellow-green or green after sporulation; phialides are morphologically diverse, single on the aerial hyphae or verticillate on the conidiophores; conidia are smooth, oval to columnar, spherical to subspherical, ovoid, aggregated in chains or clusters (Liang 2007). The typical characteristics of *M. puerense* were solitary to multiple stromata and smooth-walled, brownish in colour and producing a large number of green powdery conidia at the tip.

*Metarhizium* species that parasitise lepidopteran larvae were collected from Yunnan for this investigation. Phylogenetic location was elucidated, based on Bayesian Inference (BI) and Maximum Likelihood (ML) analyses, which involved concatenating sequences of the six loci. The results revealed that the species in question belong to the genus *Metarhizium*, specifically *Metarhizium puerense*.

# Materials and methods

#### Collection and isolation of strains

Specimens were collected from the broad-leaved evergreen forest of Pu'er, Yunnan Province, China, 2 August 2023, 22°71.33'E, 100°95.57'N, alt. 1358 m. The samples were preserved in sterile tubes and stored at 4°C. To obtain pure cultures, fresh specimens were cleaned and surface-sterilised by soaking in 30% hydrogen peroxide for approximately one minute. The samples were then washed with sterile water to remove residual hydrogen peroxide and the residual water was aspirated with a sterile filter paper. The worms were dissected on an ultra-clean bench, picked up with a sterilised scalpel with an appropriate amount of white tissue in the sclerotium centre, inoculated on potato dextrose agar medium (PDA: fresh potato 200 g/l, dextrose 20 g/l and agar 18 g/l) (Wang et al. 2020) and allowed to incubate at room temperature. The collected specimens were placed in the Yunnan Herbarium of the Yunnan University (YHH). The obtained strains were preserved at the Yunnan Fungal Culture Conservation Center (YFCC).

#### Morphological characterization

Fresh specimens, including the stromata and hosts, were photographed using a Canon 750D camera. For descriptions of colony appearance and microscopic features, the colonies on PDA plates were cultured for two weeks and the colony characteristics (size, texture and colour) were photographed with a Canon 700D camera to characterise the morphology of the colonies. Observations, measurements and photographs of the phialides and conidia were obtained using a light microscope (Olympus BX53).

#### DNA extraction, PCR and sequencing

DNA extraction was performed using a ZR Fungal DNA kit (Zymo, California, USA). DNA was preserved at -20°C and used as a template for PCR amplification of the six loci. To amplify the largest and second-largest subunit sequences of RNA polymerase II (*RPB1* and *RPB2*), the primer pair RPB1-5'F and RPB1-5'R, as well as the primer pair RPB2-5'F and RPB2-5'R, were applied (Bischoff et al. 2006). The nuclear ribosomal small and large subunits (nr*SSU* and nr*LSU*) were amplified using the primer pairs used by 18S-CoF and 18S-CoR (Wang et al. 2015), as well as LR5 and LR0R (Vilgalys and Hester 1990 and Rehner and Samuels 1994). The translation elongation factor 1 $\alpha$  (*EF-1a*) gene was amplified using the primer pair *EF1\alpha-EF* and *EF1\alpha-ER* (Bischoff et al. 2006 and Sung et al. 2007). PCR primers used to amplify the internal transcribed spacers were ITS4 and ITS5 (White et al. 1990). All PCR reactions were performed in a final volume of 50 µl and contained 25 µl of 2× Taq PCR Master Mix (Tiangen, Beijing, China), 0.5 µl forward and reverse primers (10 µM), 1 µl template DNA (1 ng/µl) and 23 µl sterile distilled water. The polymerase chain reaction (PCR) was performed as described by Wang et al. (2015).

#### Phylogenetic analysis

The data matrix included 72 sequences from 48 species in *Metarhizium* and two outgroup taxa. Sequences of six loci (ITS, nr*SSU*, nr*LSU*, *EF-1a*, *RPB1* and *RPB2*) were retrieved from GenBank. Sequences were aligned using MUSCLE software (Tamura et al. 2013). After alignment, the gene sequences were concatenated. *Clonostachys rosea*  (GJS 90-227) and *Hydropisphaera peziza* (CBS 102038) were designated as the outgroup taxa. Phylogenetic analyses were conducted using BI and ML methods with MrBayes v.3.1.2 and RaxML 7.0.3, respectively (Ronquist and Huelsenbeck 2003 and Stamatakis et al. 2008). The GTR+G+I model was determined using jModelTest version 2.1.4 (Darriba et al. 2012) with five million generations for the BI analysis. GTR+I was selected as the optimal model for the ML analysis and 1,000 rapid bootstrap replicates were performed on the dataset.

# Taxon treatment

## Metarhizium puerense Hong Yu bis, J.M. Ma & Z.Q. Wang, sp. nov.

• MycoBank <u>852903</u>

#### Materials

#### Holotype:

a. scientificName: *Metarhizium puerense* sp. nov.; country: China; stateProvince: Yunnan; locality: Pu'er City, Simao District; verbatimElevation: 1358 m; verbatimLatitude: 22°71.33'E; verbatimLongitude: 100°95.57'N; year: 2023; month: August; day: 2; identifiedBy: Hong Yu bis; institutionID: YHH MP2308031; collectionID: YFCCMP 9458; occurrenceID: 5C808899-7FA6-5C36-8FA2-DBD6D69DBD82

#### Other materials:

- a. scientificName: *Metarhizium puerense* sp. nov.; country: China; stateProvince: Yunnan; locality: Pu'er City, Simao District; verbatimElevation: 1358 m; verbatimLatitude: 22°71.33'E; verbatimLongitude: 100°95.57'N; year: 2023; month: August; day: 2; identifiedBy: Hong Yu bis; institutionID: YHHMP 2308032; collectionID: YFCCMP 9459; occurrenceID: E7C934B3-11EC-5ED2-A85F-CF9975A5C5E4
- scientificName: Metarhizium puerense sp. nov.; country: China; stateProvince: Yunnan; locality: Pu'er City, Simao District; verbatimElevation: 1359 m; verbatimLatitude: 22°71.33'E; verbatimLongitude: 100°95.57'N; year: 2023; month: August; day: 2; identifiedBy: Hong Yu bis; institutionID: YHHMP 2308033; occurrenceID: D72AACD2-AF02-550B-8D65-667FC7E27EB7

## Description

Sexual morph: Sexual morphs were not found.

**Asexual morph:** Stroma arising from the larvae of Lepidoptera larva buried in soil, solitary or multiple, brownish in colour and producing a large number of green powdery conidia at the tip. Colonies on PDA grew at 25°C, reaching 25-28 mm diam. in 14 days, cottony with high mycelium density, white to light yellow and reverse yellow; 45-52 mm in diameter in 30 days at 25°C, first white turning to green, powdery while sporulating, white mycelium at the margin. Hyphae septate, smooth-walled. Conidiophores smooth, cylindrical and erect. Phialides cylindrical, borne singly on aerial mycelium or whorled on conidial peduncle, 6.1-17.6 × 1.5-2.9  $\mu$ m. Conidia

were smooth-walled, ellipsoid to columnar, rounded at the tip, aggregated into chains or clusters,  $3.8-7.1 \times 1.3-2.1 \ \mu m$  (Fig. 1).

**Notes:** Phylogenetically, *Metarhizium puerense* is closely related to *M. album*, but differs in morphological characteristics. The morphological characteristics of *M. puerense* are as follows: stroma arising from the larva of Lepidoptera buried in soil, solitary or multiple, brownish in colour and producing a large number of green powdery conidia at the tip. *Metarhizium album* was collected from plants and leafhoppers (Homoptera, Auchenorrhyncha) from rice. Moreover, *M. puerense* was indicated by its conidia size  $(3.8-7.1 \times 1.3-2.1 \ \mu\text{m})$ , which was smaller than that of *M. album* (5-8 × 2-2.5 \ \mum). The phialides of *M. puerense* (6.1-17.6 × 1.5-2.9 \ \mum) was more slender than *M. album* (10-12.5 × 2-3.5 \ \mum) (Michiel et al. 1987). Morphological comparisons of Metarhizium puerense with its related species (Table 2).

## Etymology

Named after Pu'er City, where the species were first collected.

# Analysis

These 49 taxa were used for phylogenetic analyses (Table 1). The combined six-locus dataset contained 4862 base pairs (bp) of sequences after alignment: 607 bp for ITS, 914 bp for nr*SSU*, 802 bp for nr*LSU*, 902 bp for *EF-1a*, 688 bp for *RPB1* and 1101 bp for *RPB2*. *Clonostachys rosea* (GJS 90227) and *Hydropisphaera peziza* (CBS 102038) were designated as outgroup taxa in the phylogenetic tree. In phylogenetic trees based on both Bayesian Inference (BI) and Maximum Likelihood (ML) analyses, the samples collected in Yunnan formed a strongly-supported clade that was sister to *M. album* (BI posterior probability = 1.00, ML bootstrap =100%). This result indicates that it is a new species of *Metarhizium*, named *M. puerense* (Fig. 2).

# Discussion

To date, multi-locus phylogenetics, based on the joint analysis of ribosomal DNA and functional protein-coding genes, have been widely used in the phylogenetic study of fungi and have achieved many results (Sung et al. 2007 and Luangsa-ard et al. 2017 and Mongkolsamrit et al. 2020). In this study, we conducted an investigation, searched for and retrieved the *Metarhizium* nuclear gene sequences from the NCBI database. Subsequently, the sequences were compared with the obtained data. Additionally, a phylogenetic tree was constructed, based on multilocus database analyses (ITS, nr*SSU,* nr*LSU, EF-1a, RPB1* and *RPB2*) to elucidate the phylogenetic position of *M. puerense*. Phylogenetically, *Metarhizium puerense* is closely related to *M. album*. However, in terms of morphological characteristics, *M. puerense* parasitises the larvae of Lepidoptera, either solitary or multiple and produces a large number of green conidia. There were also differences in the sizes of phialides and conidia.

In the forests of Pu'er City, Yunnan Province, China, which are characterised by a warm and humid climate, a diverse array of entomopathogenic fungi thrive. Amongst these, *Metarhizium* is a fungal insecticide with large-scale production capabilities. It offers significant value owing to its environment-friendly nature, extended efficacy period and low resistance potential. This makes it an important asset for pest control. Hence, it is crucial to accurately identify the *Metarhizium* species and determine their host range to facilitate the development and utilisation of this potent insecticidal agent. In the current study, a new species collected from Pu'er City, *Metarhizium puerense*, is described. The phylogenetic and morphological evidence presented in this study supports the classification of the species as a new taxon within the genus *Metarhizium*. This research contributes to the expansion of diversity within *Metarhizium* species, enhances our understanding of host interactions, morphology, distribution and pure culture characteristics and provides valuable taxonomic and phylogenetic information for further detailed investigations of the genus. Additionally, this opens up new possibilities for the development of fungal insecticides.

In the investigation of entomogenous fungi resources in Yunnan, a new species of *Metarhizium* was discovered and identified. This work not only increases the diversity of species in the genus *Metarhizium*, enriches the biological fungal species resource pool in Yunnan Province, but also lays a certain foundation for the distribution of *Metarhizium* species in Yunnan Province and other regions in China. Additionally, it deepened our understanding of the morphology, distribution and pure culture characteristics of the *Metarhizium* genus and provided taxonomic and phylogenetic information for a more detailed study of the genus's systematics.

# Acknowledgements

This study was funded by the National Natural Science Foundation of China (31870017).

# References

- Bischoff JF, Rehner SA, Humber RA (2006) *Metarhizium frigidum* sp. nov.: a cryptic species of *M. anisopliae* and a member of the *M. flavoviride* complex. Mycologia 98: 737-745. <u>https://doi.org/10.1080/15572536.2006.11832645</u>
- Bischoff JF, Rehner SA, Humber RA (2009) A multilocus phylogeny of the *Metarhizium* anisopliae lineage. Mycologia 101: 512-530. <u>https://doi.org/10.3852/07-202</u>
- Chen ZH, Xu L, Yang XN, Zhang YG (2018a) *Metarhizium baoshanense* sp. nov., a new entomopathogen fungus from southwestern China. Pakistan Journal of Zoology 50 (5): 1739-1746. <u>https://doi.org/10.17582/journal.pjz/2018.50.5.1739.1746</u>
- Chen ZH, Yang XN, Sun NJ, Xu L (2018b) Species diversity and vertical distribution characteristics of *Metarhizium* in Gaoligong Mountains, southwestern China. Biodiversity Science 26 (12): 1308-1317. https://doi.org/10.17520/biods.2018131

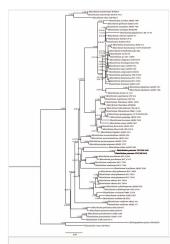
- Chen ZH, Zhang YG, Yang XN, Liu Q (2018c) A new fungus *Metarhizium gaoligongense* from China. International Journal of Agriculture & Biology 20 (10): 2271-2276. <u>https:// doi.org/10.17957/IJAB/15.0777</u>
- Chen ZH, Dai YD, Chen K, Zhang YF (2023) *Papiliomyces puniceum* and *Metarhizium lymantriidae*: two new species from the Gaoligong Mountains in southwestern China. Phytotaxa 594 (1): 053-063. <u>https://doi.org/10.11646/phytotaxa.594.1.3</u>
- Darriba D, Taboada GL, Doallo R, Posada D (2012) jModelTest 2: Moremodels, new heuristics and parallel computing. Nature Methods 9 (8): 772-772. <u>https://doi.org/10.1038/</u> <u>nmeth.2109</u>
- Driver F, Milner RJ, Trueman JW (2000) A taxonomic revision of *Metarhizium* based on a phylogenetic analysis of rDNA sequence data. Mycological Research 104: 134-150. <u>https://doi.org/10.1017/S0953756299001756</u>
- Kepler RM, Sung GH, Chen MJ, Spatafora JW (2012) New teleomorph combinations in the entomopathogenic genus *Metacordyceps*. Mycologia 104: 182-197. <u>https://doi.org/ 10.3852/11-070</u>
- Kepler RM, Humber RA, Bischoff JF, Rehner SA (2014) Clarification of generic and species boundaries for *Metarhizium* and related fungi through multigene phylogenetics. Mycologia 106: 811-829. <u>https://doi.org/10.3852/13-319</u>
- Liang Z (2007) Annals of Chinese Fungi. 3. ZQ Liang
- Li Y, Zhao XC, Wu LX, Wang Y (2023) Blackwellomyces kaihuaensis and Metarhizium putuoense (Hypocreales), two new entomogenous fungi from subtropical forests in Zhejiang Province, Eastern China. Forests 14 (12): 2333. <u>https://doi.org/10.3390/f14122333</u>
- Luangsa-ard JJ, Mongkolsamrit S, Thanakitpipattana D, Khonsanit A (2017) Clavicipitaceous entomopathogens: new species in *Metarhizium* and a new genus *Nigelia*. Mycological Progress 16 (4): 369-391. <u>https://doi.org/10.1007/s11557-017-1277-1</u>
- Michiel CR, Richard AH, Harry CE (1987) *Metarhizium album*, a fungal pathogen of leafand planthoppers of rice. <u>Transactions of the British Mycological Society</u> 88 (4): 451-459. <u>https://doi.org/10.1016/S0007-1536(87)80028-1</u>
- Mongkolsamrit S, Khonsanit A, DThanakitpipattana, Tasanathai K (2020) Revisiting *Metarhizium* and the description of new species from Thailand. Studies in Mycology 95: 171-251. <u>https://doi.org/10.1016/j.simyco.2020.04.001</u>
- Rehner SA, Samuels GJ (1994) Taxonomy and phylogeny of *Gliocladium* analysed from nuclear large subunit ribosomal DNA sequences. Mycological Research 98 (6): 625-634. https://doi.org/10.1016/S0953-7562(09)80409-7
- Ronquist F, Huelsenbeck JP (2003) MrBayes 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 19 (12): 1572-157. <u>https://doi.org/10.1093/bioinformatics/ btg180</u>
- Stamatakis A, Hoover P, Rougemont J (2008) A rapid bootstrap algorithm for the RAxML Web servers. Systematic Biology 57 (5): 758-771. <u>https://doi.org/</u> <u>10.1080/10635150802429642</u>
- Sung GH, Hywel-Jones NL, Sung JM (2007) Phylogenetic classification of *Cordyceps* and the clavicipitaceous fungi. Studies in Mycology 57: 5-59. <u>https://doi.org/10.3114/sim.</u> 2007.57.01
- Tamura K, Stecher G, Peterson D, Filipski A (2013) MEGA6: molecular evolutionary genetics analysis version 6.0. Molecular Biology and Evolution 30: 2725-2729. <u>https:// doi.org/10.1093/molbev/mst197</u>

- Tulloch M (1976) The genus *Metarhizium*. Transaction of the British Mycological Society 66: 407-411. <a href="https://doi.org/10.1016/S0007-1536(76)80209-4">https://doi.org/10.1016/S0007-1536(76)80209-4</a>
- Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cyptococcus* species. Journal of Bacteriology 172 (8): 4238-4246. <u>https://doi.org/10.1128/jb.172.8.4238-4246.1990</u>
- Wang Y, Tang D, Duan D, Wang Y (2020) Morphology, molecular characterization, and virulence of *Beauveria pseudobassiana* isolated from different hosts. Journal of Invertebrate Pathology 172: 107333. <u>https://doi.org/10.1016/j.jip.2020.107333</u>
- Wang YB, Yu H, Dai YD, Wu CK (2015) *Polycephalomyces agaricus*, a new hyperparasite of *Ophiocordyceps* sp. infecting melolonthid larvae in southwestern China. Mycological Progress 14: 70. <u>https://doi.org/10.1007/s11557-015-1090-7</u>
- White TJ, Bruns T, Lee S, Taylor JW (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: PCR protocols: a guide to methods and applications (Innis MA, Gelfand DH, Sninsky JJ, White TJ, eds). Academic Press, New York315-322. <u>https://doi.org/10.1016/B978-0-12-372180-8.50042-1</u>



#### Figure 1.

*Metarhizium puerense* (YFCCMP 9458). **A** Stromata arising from hosts buried in soil; **B** Fungus on the larvae of Lepidoptera; **C** Apical part of stromata; **D-E** Culture characters on PDA (**D** = after 14 days, **E** = after 30 days). **F-I**. Conidiophores, phialides and conidia; **J-K** Conidia. Scale bars: **A-E** = 1 cm. *F-J* = 10  $\mu$ m. **K** = 5  $\mu$ m.



## Figure 2.

Phylogenetic placement of *M. puerense* was inferred from Maximum Likelihood (ML) and Bayesian Inference (BI) analyses, based on six loci (ITS, nr*SSU*, nr*LSU*, *EF-1a*, *RPB1* and *RPB2*).

## Table 1.

GenBank accession numbers of materials used in this study.

Metarhizium acridum	ARSEF 7486	Orthoptera	HQ331458			EU248845	EU248897	EU248
Metarhizium album	ARSEF 2082	Hemiptera	AY375446	DQ522560	DQ518775	DQ522352	KJ398617	KJ3987
Metarhizium alvesii	CG 1123	Soil				KY007614	KY007612	KY0076
Metarhizium anisopliae	ARSEF 7487	Orthoptera	HQ331446			DQ463996	DQ468355	DQ468
Metarhizium anisopliae	BUM 1900	Soil	MH143803	MH143837	MH143820	MH143854	MH143869	MH143
Metarhizium argentinense	CEP 414	Blattodea: Blaberidae ( <i>Epilampra</i> sp.)	MF784813			MF966620	MF966621	MF966
Metarhizium argentinense	CEP 424	Blattodea: Blaberidae ( <i>Epilampra</i> sp.)				MF966624	MF966625	MF966
Metarhizium baoshanense	BUM 63.4	Soil	KY264173	KY264178	KY264175	KY264170	KY264181	KY2647
Metarhizium baoshanense	CCTCCM2016589	Soil	KY264172	KY264177	KY264174	KY264169	KY264180	KY2647
Metarhizium bibionidarum	CBS 648.67	Coleoptera: Scarabaeidae ( <i>Cetonia</i> <i>aurata</i> )				LC126075	LC125907	LC1259
Metarhizium bibionidarum	NBRC 112661	Diptera (March fly larva)				LC126076	LC125908	LC1259
Metarhizium blattodeae	ARSEF 12850	Blattodea: Ectobiidae	KU182915			KU182917	KU182918	KU1829
Metarhizium blattodeae	MY00896	Blattodea	HQ165697	HQ165657	HQ165719	HQ165678	HQ165739	HQ165
Metarhizium brachyspermum	CM1	Coleoptera	LC469747		LC469749	LC469751		
Metarhizium brasiliense	ARSEF 2948	Hemiptera	AF139854			KJ398809	KJ398620	KJ3987
Metarhizium brittlebankisoides	Hn1	Coleoptera				AB778556	AB778555	AB778
Metarhizium brunneum	ARSEF 2107T	Coleoptera	KC178691		MH868397	EU248855	EU248907	EU248
Metarhizium campsosterni	BUM 10	Soil	MH143798	MH143832	MH143815	MH143849	MH143864	MH143
Metarhizium chaiyaphumense	BCC 19020	Hemiptera: Cicadidae (cicada adult)	HQ165695	HQ165654	HQ165716	HQ165675	HQ165737	HQ165
Metarhizium chaiyaphumense	BCC 19021	Hemiptera: Cicadidae (cicada nymph)	HQ165696	HQ165655	HQ165717	HQ165676	HQ165738	HQ165

Metarhizium chaiyaphumense	BCC 78198	Hemiptera: Cicadidae (cicada nymph)		KX369596	KX369593	KX369592	KX369594	KX369
Metarhizium cylindrosporum	ARSEF 6926	Hemiptera				KJ398814	KJ398625	KJ3987
Metarhizium cylindrosporum	CBS 256.90	Hemiptera	MH862209		MH873892	KJ398783	KJ398594	KJ3986
Metarhizium flavoviride	ARSEF 2025	Soil	AF138269			KJ398804	KJ398614	KJ3987
Metarhizium flavoviride	CBS 218.56	Coleoptera	MH857590		MH869139	KJ398787	KJ398598	KJ3986
Metarhizium frigidum	ARSEF 4124	Coleoptera	HM055448			DQ464002	DQ468361	DQ468
Metarhizium gaoligongense	CCTCCM2016588	Soil	KY087808	KY087812	KY087816	KY087820	KY087824	KY0878
Metarhizium globosum	ARSEF 2596	Lepidoptera	HQ331459			EU248846	EU248898	EU248
Metarhizium granulomatis	UAMH 11028	Chamaeleo calyptratus	HM195305	HM635076	HM195304	KJ398781		KJ3986
Metarhizium granulomatis	UAMH 11176	Chamaeleo calyptratus	HM195306		HM635078	KJ398782	KJ398593	KJ3986
Metarhizium guizhouense	CBS 258.90	Lepidoptera larva	MH862211		MH873894	EU248862	EU248914	EU248
Metarhizium humberi	IP 46	Soil				MH837574	MH837556	MH837
Metarhizium humberi	IP 86	Soil				MH837576	MH837558	MH837
Metarhizium indigoticum	TNS F18553	Lepidoptera Iarva	JN049874	JF415952	JF415968	JF416010	JN049886	JF4159
Metarhizium kalasinense	BCC 53581	Coleoptera Iarva	KC011178	KC011174	KC011182	KC011188		
Metarhizium kalasinense	BCC 53582	Coleoptera Iarva	KC011179	KC011175	KC011183	KC011189		
Metarhizium koreanum	ARSEF 2038	Hemiptera	HM055431			KJ398805	KJ398615	KJ3987
Metarhizium lepidiotae	ARSEF 7412	Coleoptera	HQ331455			EU248864	EU248916	EU248
Metarhizium lepidiotae	ARSEF 7488	Coleoptera	HQ331456			EU248865	EU248917	EU248
Metarhizium Iymantriidae	BUM 818		OM955147	OM951242	OM951247	OM988196	OM988192	OM988
Metarhizium Iymantriidae	KUNCC 4991		OM955148	OM951243	OM951248	OM988197	OM988193	-
Metarhizium majus	ARSEF 1914	Coleoptera	HQ331445			EU248868	EU248920	EU248
Metarhizium majus	ARSEF 1946	Coleoptera	HM055450			EU248867	EU248919	EU248
Metarhizium minus	ARSEF 2037	Hemiptera	AF138271	AF339580	AF339531	DQ522353	DQ522400	DQ522
Metarhizium novozealandicum	ARSEF 3056	Soil				KJ398810	KJ398621	KJ3987

Metarhizium novozealandicum	ARSEF 4661	Soil				KJ398811	KJ398622	KJ3987
Metarhizium owariense	NBRC 33258	Hemiptera	JN049883	HQ165669	HQ165730	JF416017	KJ398596	JF4159
Metarhizium pemphigi	ARSEF 6569	Hemiptera: Apididae	-	-	-	KJ398813	KJ398624	KJ3987
Metarhizium pinghaense	CBS 257.90	Coleoptera	HQ331450	-	MH873893	EU248850	EU248902	EU248
Metarhizium prachinense	BCC 47950	Lepidoptera	KC011176	KC011172	KC011180	KC011186	KC011184	-
Metarhizium prachinense	BCC 47979	Lepidoptera	KC011177	KC011173	KC011181	KC011187	KC011185	-
Metarhizium purpureogenum	ARSEF 12570	Soil				LC126079	LC125911	LC1259
Metarhizium purpureogenum	ARSEF 12571	Soil			AB700552	LC126078	LC125913	LC1259
Metarhizium putuoense	HMAS 285457	Coleoptera (larva)		OQ981977	OQ981970	OQ980403	OQ980411	
Metarhizium putuoense	HMAS 285457	Coleoptera (larva)		OQ981978	OQ981971	OQ980404	OQ980412	
Metarhizium puerense	YFCCMP 9458	Lepidoptera	PP733948	PP733950	PP733952	PP776150	PP776152	PP776 <sup>/</sup>
Metarhizium puerense	YFCCMP 9459	Lepidoptera	PP733949	PP733951	PP733953	PP776151	PP776153	PP776
Metarhizium reniforme	ARSEF 429	Orthoptera	DQ069284	HQ165671	HQ165733	HQ165690		HQ165
Metarhizium reniforme	ARSEF 577	Orthoptera: Tettigoniidae	DQ069283	HQ165672	HQ165734	HQ165691		HQ165
Metarhizium rileyi	CBS 806.71	Lepidoptera: Noctuidae ( <i>Trichoplusia</i> <i>ni</i> )	AY624205	AY526491	MH872111	EF468787	EF468893	EF4689
Metarhizium robertsii	ARSEF 727	Orthoptera	HQ331453			DQ463994	DQ468353	DQ468
Metarhizium samlanense	BCC 17091	Hemiptera: Cicadellidae (adult)	HQ165707	HQ165665	HQ165727	HQ165686		HQ165
Metarhizium samlanens e	BCC 17093	Hemiptera: Cicadellidae (adult)	HQ165709	HQ165666	HQ165728	HQ165687	HQ165746	HQ165
Metarhizium takense	BCC 30934	Hemiptera: Cicadidae (cicada nymph)	HQ165698	HQ165658	HQ165720	HQ165679	HQ165740	HQ165
Metarhizium takense	BCC 30939	Hemiptera: Cicadidae (cicada nymph)	HQ165699	HQ165659	HQ165721	HQ165680	HQ165741	HQ165
Metarhizium viride	CBS 659.71	Hemiptera: Cicadidae (cicada nymph)	HQ165714	HQ165673	HQ165735	HQ165692		HQ165

Metarhizium viridulum	ARSEF 6927	Chamaeleo Iateralis				KJ398815	KJ398626	KJ3987
Metarhizium viridulum	BUM 721	Hemiptera	MH143808	MH143842	MH143825	MH143859	MH143874	MH1438
Metarhizium taii	KS 50	Soil		GU979940-	GU979949	GU979958		GU9799
<i>Metarhizium</i> sp.	OSC 110996			EF468974	EF468832	EF468773	EF468880	EF4689
Clonostachys rosea	GJS 90-227			AY489684	AY489716	AY489611		
Hydropisphaera peziza	CBS 102038			AY489698	AY489730	AY489625	AY489661	DQ5224

## Table 2.

Morphological comparisons of *Metarhizium puerense* with its related species.

Species	Host	Stromata	Fertile part	Colony on PDA	Anamorph	P hialides (µm)	Conidia (µm)	Referenc
M . puerense	Lepidoptera larva	Solitary or multiple, 2.6–4.7 cm long, 1.2–1.5 mm broad	Cylindrical to clavate, contains a large number of green conidia, 1–2 cm long, 1– 1.5 mm broad	White dense mycelium, producing green spores later	Chain shape, clumping together	Solitary or in whorls of 2, 6.1– 17.6 × 1.5–2.9	Ovoid to elliptical, 3.8– 7.1 × 1.3–2.1	This stud
M. album	Leafhoppers			Pure white to yellowish white, or greyish white becoming pinkish to fawn to pale brown upon sporulation	Conidial chains	Clavate phialides, solitary or in whorls of $2-5,10-12.5 \times 2-3.5$	Narrowly ellipsoid or ovoid, (3–)4–6 × I.5–2.5	Michiel et al. (1987)
M. brasiliense	Leafhoppers (Hemiptera: Cicadellidae)			White to cream, becoming dark green to bluish green			Short conidia, 5.5–9 × 2.5–3.5	Kepler et (2014)
M. samlanense	Leafhoppers (Hemiptera: Cicadellidae)			At first white turning green due to conidiation	Conidial chains	Phialides are short and cylindrical, 5–7 × 2–3	Green, globose, 3 × 5	Luangsa- ard et al. (2017)
M. prachinense	Lepidoptera larva	Stromata usually branched, 50–86 × 1–2 mm, broad	Cylindrical with pointed ends, white, pale yellow to grayish yellow, 0.8–1.7 × 1 mm	Initially colorless, turning green due to the production of green conidia	Conidial chains	Ovoid to obpyriform with short distinct neck, $3-5 \times 2$	Subglobose, green, 3–5 × 1.5–2.5	Luangsa- ard et al. (2017)